

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2000, 20:18:59 ; Search time 67.51 Seconds
(without alignments)
444.374 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQTATSPDGGTTFEHLWS.....PDCAKRKQIKKEFTAEIHH 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_62.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851.5	25.2	396	1 JH0631	cellular tumor ant
2	778	23.0	367	1 S02193	cellular tumor ant
3	760.5	22.5	386	1 S11648	cellular tumor ant
4	749	22.1	396	1 JH0633	cellular tumor ant
5	741.5	21.9	393	2 JG6176	tumor suppressor p
6	741.5	21.9	363	1 A39376	cellular tumor ant
7	735.5	21.7	391	1 S02192	cellular tumor ant
8	724.5	21.4	391	2 JG6193	tumor suppressor p
9	724.5	21.4	393	1 DNH53	cellular tumor ant
10	718.5	21.2	393	1 S06594	cellular tumor ant
11	711.5	21.0	390	1 DNH53	cellular tumor ant
12	702	20.7	381	2 S38824	cellular tumor ant
13	248.5	7.3	77	2 I46226	p3 - dog (fragmen
14	151.5	4.5	903	2 T00074	hypothetical prote
15	145	4.3	864	2 T04518	hypothetical prote
16	139.5	4.1	1221	2 T13283	probable transcrip
17	133	3.9	1273	2 S58782	SFC31 protein - ye
18	131.5	3.9	2364	2 A56577	microtubule-associ
19	129	3.8	306	2 A4354	extensin precursor
20	127.5	3.8	784	2 S26638	SPR-1 protein - hu
21	126	3.7	817	2 S1342	verprolin - yeast
22	126	3.7	1791	2 T02909	hypothetical prote
23	125.5	3.7	1560	2 T02885	peroxisome prolif
24	125	3.7	1081	2 T13231	dachshund protein
25	124.5	3.7	2397	1 A55335	vesican precursor
26	124	3.7	650	2 T04487	hypothetical prote
27	124	3.7	1051	1 JW0051	serine/threonine-s
28	124	3.7	1099	2 A56155	tumor suppressor p
29	123.5	3.6	1618	2 S21424	nestin - human
30	123	3.6	1065	2 T13230	dachshund isoform

transcription acti
CREB-binding prote
CREB-binding prote
eyelid - fruit fly
dachshund protein
dachshund protein
translation initia
capsid protein - h
protein p130 - rat
ALR protein - huma
ALR protein - huma
transcription acti
tight junction pro
hydroxyproline-ric

31 123 3.6 1638 2 A42091
32 123 3.6 2440 2 S39162
33 123 3.6 2441 2 S39161
34 123 3.6 2715 2 T13049
35 122.5 3.6 1072 2 T13228
36 122.5 3.6 1072 2 T13232
37 122 3.6 1074 2 T13229
38 122 3.6 1396 2 A44453
39 118.5 3.5 635 1 WNBW6
40 118.5 3.5 968 2 S46992
41 118.5 3.5 4957 2 T03455
42 118.5 3.5 5262 2 T03454
43 118 3.5 1081 2 S66736
44 118 3.5 1736 2 A47747
45 116 3.4 620 2 S06733

ALIGNMENTS

RESULT 1

JH0631

cellular tumor antigen p53 - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 10-Sep-1989 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0631

R:de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.

Gene 112, 241-245, 1992

A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.

A:Reference number: JH0631; MUID:92210006

A:Accession: JH0631

A:Molecule type: mRNA

A:Residues: 1-396 <DEF>

A:Cross-references: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829

A:Experimental source: liver

C:Comment: This protein is the product of a tumor suppressor gene, p53, whose ir

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus

F.164, 167, 227, 231/Binding site: zinc (Cys, His, Cys, Cys); #status predicted

F.395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 25.2% Score 851.5; DB 1; Length 396;

Best Local Similarity 55.6%; Pred. No. 4.9e-52;

Matches 170; Conservative 43; Mismatches 86; Indels 7; Gaps 5;

QY 93 VPTHSPYAQPS-STFDIMS-PAPVPSNTDYPGPHFEVTFQSSSTAKSATWYSPLLKK 150

DB 61 VSATEPAPQPSISTDTGSPPTSTVPTSDPGALGFQLRFLQSSSTAKSVTCTYSPDLNK 120

QY 151 LYCQAKTCPTQIKVSPPPPGTAIRAMPVYKKAHVTDVVKPCPNHGLGRDFNEQSAP 210

DB 121 LFCQLAKTCPTQIVVDHPFPGAVRALAIYKLLSDVADVVRCPHQHQTSENNEG-PAP 179

QY 211 ASHLIRVGNLSDYDPTVGRSVVYPPVPPVQVTEFTILYFNMCSSCVGGMNRRP 270

DB 180 RGLHVRVGNORSEYMEDGNTLRHSLVLPVYPPVQVSECTVLYFNMCSSCMGGMNRRP 239

QY 271 ILIITLMDRGVLRSGREGICACPGDRKADHDHYEQOALN-ESSAKNGAASRA 329

DB 240 ILIITLMDRGVLRSGREGICACPGDRKADHDHYEQOALN-ESSAKNGAASRA 299

QY 330 FKQSPVAPALGAGVKKRRH---GDETTYLVQVRGNFELMKLESLELMELVPOPLV 386

DB 300 MKEASLPAPQPGASKTKSSPAVSDDEIYTLQIRGEKYEMLKKFNDSLELSLPVADA 359

QY 387 DSYRQQ 392

DB 360 DKYRQK 365

RESULT 2

S02193

cellular tumor antigen p53 - chicken
N:Alternate names: nuclear oncoprotein p53
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Soussi, T.; Beque, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A:Reference number: S02193; MUID:89083584
A:Accession: S02193
A:Molecule type: mRNA
A:Residues: 1-367 <SD>
A:Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
F:161,164,224,228/Binding site: zinc (Cys, His, Cys) #status predicted
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 23.0%; Score 778; DB 1; Length 367;
Best Local Similarity 44.1%; Pred. No. 5.8e-47;
Matches 164; Conservative 56; Mismatches 106; Indels 46; Gaps 7;
QY 15 FEHLWSLEPDSITYFDLPSSRGNNVYGGTSSMDVPHLEGMTTSVMAOFNLLSSTMQ 74
Db 15 FMDLWSMLPYSMOQLPLPDHSHWOEL-----SPLEP 46
QY 75 MSSRAASAPYTPPEHAASVPTSPAPQSSFTDMSRAPVTPSNTDYPGPHHEVTFQOS 134
Db 47 SDPPPPPPPPPLPLAANPPPLNPTTPRA-----APSPVPTSDYGGDFRVGFVEA 101
QY 135 STAKSATWTSYLLKLYCQIAKTCPIQIKYSTPTPPPGTAIRAMPVYKKAHVTDVVKRC 194
Db 102 GTAKSTCYTSPVNLKVCRLAKCPQVRGVGAPPDGSLSRAVAVYKKEHAEVVRRC 161
QY 195 PNEHGRDNEGQSPASHLIRVEGNNSQVVDVPGVGRQSVVYVPPQVGTFTILY 254
Db 162 PHHERCGGTG-D-LAPAOHLIRVEGNPOARYHDDTKRHVSVVYVYVPPVGVSDCTVLY 220
QY 255 NFNCSNCGVGNRRPILIIILEMRDQVIGRSGFEGRICACPRDKADEHYREOQA 314
Db 221 NFNCSNCGVGNRRPILITILEGQGLGRCFEVRVACPRDKKEEFENFRKRG 280
QY 315 LNESSAKGAASKRAFKSPAPVAPGALGAVYKRRHGDDETYILOVRGRENFEILMKLKS 374
Db 281 A-----GGVAKRA--NSPP-TEAPPPKKRVLPDNEIFYLQVRGRRRYEMKLKINEA 330
QY 375 LEIWE--LVPOP 384
Db 331 LQAEGGSAPRP 342

RESULT 3
S51648
cellular tumor antigen p53 - bovine
N:Alternate names: tumor-suppressor protein p53
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Dequiedt, F.; Willens, L.; Burny, A.; Kettmann, R.
submitted to the EMBL Data Library, September 1994
A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its g
A:Reference number: S51648
A:Accession: S51648
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-386 <DEQ>
A:Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
F:168,171,231,235/Binding site: zinc (Cys, His, Cys) #status predicted
F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 22.5%; Score 760.5; DB 1; Length 386;
Best Local Similarity 44.2%; Pred. No. 1e-45;
Matches 169; Conservative 63; Mismatches 105; Indels 45; Gaps 11;
QY 60 SYMAQFNLLSSTMDQSSRAASAPYT-----PEHAASVPTHS-PYAQPSSTFTDM 109
Db 24 NLLPENLLSS---ELSAVDLLPTVDVATVDECPNEAQPMPESAAPPPAT---- 77
QY 110 SPAPV-----IPSNTPDYPGPHHEVTFQOSSTAKSATWTSYLLKLYCQIAKTCPI 161
Db 77 -PATATSWPLSSFVPSOKTYPGNYGRFLGQSTAKSVCTYSPSLNKLFCQIAKTCPI 135
QY 162 QIKYSTPTPPPGTAIRAMPVYKKAHVTDVVKRCNHELGRDNFNEGQSPASHLIRVEGN 221
Db 136 QLWVDSPPPPGCTRVRAAIYKKEHTEVVRCPHHERSDYSDG-LAPQHLIRVEGNL 194
QY 222 LSQVVDVPGVGRQSVVYVPPQVGTFTILYFNCSNCGVGNRRPILIIILEMRD 281
Db 195 RAEYDDRNTRFHSVVVPIESPIDSECTIIHFNCSNCGVGNRRPILITILEDSC 254
QY 282 GOVLGRSFEGRICACPRDKADEHYREQ-OALNESSAKGAASKRAFKOSPPAPVAPAL 340
Db 255 GNLLGRNSFEVRVACPRDRRTTEENLRKKGSCPEPPR---STKRALPTNTSSPQ- 311
QY 341 GAGYKRRHGDDETYILOVRGRENFEILMKLESLELMELVLPQPLVDYSRQOQLLQRP 400
Db 311 ----PKKKPDGGETFLQINGFKRYEMFRELNDALDELKDAL-----DGREPGESEHSS 360
QY 401 HLOP---PSYGPVLSPMNKVHG 419
Db 361 HLKSKRPSPSCHKKPKMKREG 382

RESULT 4
JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0633
R:Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992.
A:Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH0633; MUID:92210007
A:Accession: JH0633
A:Molecule type: mRNA
A:Residues: 1-396 <LEG>
A:Cross-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
A:Experimental source: kidney, strain MP1
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:179,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 22.1%; Score 749; DB 1; Length 396;
Best Local Similarity 43.8%; Pred. No. 6.8e-45;
Matches 165; Conservative 58; Mismatches 104; Indels 50; Gaps 10;
QY 14 TFEHLWSLEPDSITYFDLPSSRGNNVYGGTSSMDVPHLEGMTTSVMAOFNLLSSTMD 73
Db 18 TFSDLKLLPPNNVLTLPSS-----DSIEELFLENVA-----GWLDPGE 59
QY 74 QMSRAASAPYTPPEHAASVPTSPAPQSSFTDMSRAPV---TPSNTPDYPGPHHF 127
Db 60 ALQGSAAAAPAP--AAEDPVAETPAPVASAPAT-----FWPLSSSVPSYKTYGQDYG 112
QY 128 EVTFQOSSTAKSATWTSYLLKLYCQIAKTCPIQIKYSTPTPPPGTAIRAMPVYKKAHV 187
Db 113 RLGLFHSHTAKSVCTYSPSLNKLFCQIAKTCPVOLVSSVTPPPGTRVRAAIYKKLQYM 172

QY 188 TDVVKRCPNHELGRDNFEGOS-APASHLIRVEGNNLSOYVDDPVTGROSVVVPYEPQVG 246
 Db 173 TEVVRCPHRS-SEGDLAPPOHLIRVEGNMHAELDDKQTFRHSVVVPYEPPEVG 229
 QY 247 TETTLTYNFMCSGCGMNRPIILITLWROGVLRGSPFGRICACPGDRRADE 306
 Db 230 SDCTTHYNYMCSGCGMNRPIILITLEDPSGNLGRNSFEVIRICACPGDRRTEE 289
 QY 307 DHVREQ-----QALNESSAKNGAARAFKQSPAPVAPALGAGVKRRHGDETYLYOVRGR 362
 Db 290 KNFQKGEPCPELPKSAKRALPTNTSSSPQ-----RKKTLDGEYFLKIRGQ 338
 QY 363 ENFEILMKLESLEME 379
 Db 339 ERFKMFQELNEALELKD 355

RESULT 5
 JC6176
 tumor suppressor protein p53 - Chinese hamster
 C:Species: Crictetus griseus (Chinese hamster)
 C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
 C:Accession: JC6176
 R:Lee, H.; Larner, J.M.; Hamlin, J.L.
 Gene 184, 177-183, 1997
 A:Title: Cloning and Characterization of Chinese hamster p53 cDNA.
 A:Reference number: JC6176; MUID:97183659
 A:Contents: liver
 A:Accession: JC6176
 A:Molecule type: mRNA
 A:Residues: 1-393 <LEE>
 A:Cross-references: GB:U50395; NID:g1842229; PIDN:AA53040.1; PID:g1842230
 C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage
 ition, and recombination by protein/protein interactions.
 C:Genetics:
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: liver; tumor

Query Match 21.98; Score 741.5; DB 2; Length 393;
 Best Local Similarity 43.7%; Pred. No. 2.2e-44;
 Matches 162; Conservative 57; Mismatches 111; Indels 41; Gaps 8;
 QY 14 TFEHLWSLEPDSYFDLPQSSRGNNNEVVGTDSDMDVPHLEGMTSVMAQNFLLSSYMD 73
 Db 18 TFSOLKLLPPNNVSLTSPS-----DSIELFSENVTGLWSDSGALQGVAA 66
 QY 74 QMSRAASAPYTPPEHAASVTPHSYPAQPSSTFTDMSAPVPSNTDYPGPHHFEVTFQ 133
 Db 67 AAATAEDPVTETPAPASAPA-TPWPLSS-----VPSYKTFQDYGFRGLFLH 115
 QY 134 SSTAKSATWYSPLLKLYCOIAKTCPIQIKVSTPPPGCTATRAMPYVYKAEHVTDYKR 193
 Db 116 SGTAQSVTCYSPSLNKLFCOLAKTCVQLWVNSTPPGTRVRAAIYKGLQYMTVEYRR 175
 QY 194 CPNHELGRDNFEGOS-APASHLIRVEGNNLSOYVDDPVTGROSVVVPYEPQVGFEFTTI 252
 Db 176 CPHRS-SEGDLAPPOHLIRVEGNLHAEVLDKQTFRHSVVVPYEPPEVSGDCTTI 232
 QY 253 LYNFMCSGCGMNRPIILITLWROGVLRGSPFGRICACPGDRRADEHYREQ 312
 Db 233 HYNMCSGCGMNRPIILITLEDPSGNLGRNSFEVIRICACPGDRRTEKNFOK 292
 QY 313 -----QALNESSAKNGAARAFKQSPAPVAPALGAGVKRRHGDETYLYOVRGRETEIL 368
 Db 293 GPCPELPKSAKRALPTNTS--SSPP-----PKKLDGEYFLKIRGHRFRMF 341
 QY 369 MKLESLEME 379
 Db 342 QELNEALELKD 352

RESULT 6

A29376
 cellular tumor antigen p53 - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A29376; S61531; S72313; S151639
 R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
 Oncogene 1, 71-78, 1987
 A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for
 A:Reference number: A29376; MUID:88143684
 A:Accession: A29376
 A:Molecule type: mRNA
 A:Residues: 1-363 <SOU>
 A:Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962
 R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
 Oncogene 9, 109-120, 1994
 A:Title: Overexpression of wild-type p53 interferes with normal development in
 A:Reference number: S151639; MUID:94134403
 A:Accession: S61531
 A:Molecule type: mRNA
 A:Residues: 1-293, 295-363 <HOE>
 A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
 R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.
 submitted to the EMBL Data Library, March 1994
 A:Reference number: S72313
 A:Accession: S72313
 A:Molecule type: mRNA
 A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOW>
 A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
 C:Genetics:
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus
 F:150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.9%; Score 741; DB 1; Length 363;
 Best Local Similarity 41.7%; Pred. No. 2.2e-44;
 Matches 169; Conservative 54; Mismatches 92; Indels 90; Gaps 12;
 QY 1 MAQSTATSP---GGTTFEHLWSLEPD-----STYFDLPQSSRGNNNEVVGTT 45
 Db 1 MEPSSETGMDPPLSQSTFTFDLSLL-PDPQTQVTCRLDNLSEFPDYPLA----- 49
 QY 46 DSSMDVPHLEGMTSVMAQNFLLSSTMDQMSRAASAPYTPPEHAASVTPHSYPAQPSST 105
 Db 49 -ADMVLIQ-EGLMGN-----AVPTVTSKA----- 71
 QY 106 FDTMSAPVPSNTDYPGPHHFEVTFQSSATAKSTWYSPLLKLYCOIAKTCPIQIKV 165
 Db 71 -----VPSTDDYAGKYLQGLDFQONGTAKSVTCYSPELNKLFCOLAKTCPLLVV 121
 QY 166 STPPPGTATRAMPYVYKAEHVTDVVKRCPNHELGRDNFEGO-SAPASHLIRVEGNNLSQ 224
 Db 122 ESPPPGSLTATAYKKEHVAEYVKKRCPHE--RSVEGEDAAPSHLMRVVEGNLQAY 179
 QY 225 YVDDPVTGROSVVVPYEPQVGFEFTTILYNFMCSGCGMNRPIILITLEDMDGOV 284
 Db 180 YMEDVNSGRHSVCVPEYEGVQGTCTTVLYNYMCSGCGMNRPIILITLETQGLL 239
 QY 285 LGRRFEGRICACPGDRRADEHYRQOQALNESSAKNGAARAFKQSPAPVAPALGAGV 344
 Db 240 LGRRCFEYVACPGDRRTEEDNYTKRGLKPS-----GRRLAHPSPSEPPPL---P 289
 QY 345 KRRR---HGDETTYLYOVRGRETEILMKLESLEMLVPOPIV 386
 Db 290 KRLVVVDDEITLIRKGRSYEMIKKLNDALELQESLDQKV 334

RESULT 7
 S02192

cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:89083585
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13038; NID:956828; PIDN:CAA31457.1; PID:956829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268
A:Accession: S41149
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173; 'W', 175-391 <HUL>
A:Cross-references: EMBL:L07909
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
F:174,177,236,240/Binding site: zinc (Cys, His, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.7%; Score 735.5; DB 1; Length 391;
Best Local Similarity 42.8%; Pred. No. 5.8e-44;
Matches 167; Conservative 55; Mismatches 87; Indels 81; Gaps 12;

QY 14 TFEHLWSLEPDSYFDLPQSSRGNEVGGTDSMDVF-----HLEGTTTSMVAFN 66
DB 18 TFSCLWKLPPDDI---LPTTA-----TGSPNSMEDLPQDVAELEG----- 59

QY 67 LLSTMDQMSRAASAPYTPPEHAASVP-THSPYAPQSTFDTMSPAPV----- 115
DB 59 -----PEALQV--SAPAAQEPG---TEAPAPAPASATPWPPLSS 93

QY 115 -IPSNIDYPGPHFEVTFQSSSTAKSATWTYSPLKLYCQIAKTCPIQIKVSTPPPGT 173
DB 94 SVPSQKYQNGYFGLGSGTAKSVMTCTYSLSLKLFCQIAKTCPIQLWSTPPPGT 153

QY 174 AIRAMPYKKAHVTDVKKCPNHELGRDFNEGQSPASHLRVSGNLSQYVDDPVTGR 233
DB 154 RVRAAIYKKSQHTVYVRCPPHERCSD-GDG-LAPPOHLIRVSGNPAEYLDROTFR 211

QY 234 QSVVVPYEPQVGTFTTILYNFMCNCCVGGNRRPILITILEMRDQGVLRGRSTFGR 293
DB 212 HSVVVPYEPVSGDITTIYKNCSSCGMGNRRPILITILEMRDQGVLRGRSTFGR 271

QY 294 ICACPGDRKADHDHREOQ-----ALNESAKNGAKRAKFPQSPAPVAPALGAGVKKRRH 349
DB 272 VCACPGDRKADHDHREOQ-----ALNESAKNGAKRAKFPQSPAPVAPALGAGVKKRRH 349

QY 350 GDETYVYLVQVRGRENPELMLKESLELME 379
DB 321 LDGEYFLKIRGRERFEMFELNEALELKD 350

RESULT 8
JC6193
tumor suppressor p53 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C:Accession: JC6193
R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.
Gene 185, 169-173, 1997
A:Title: cDNA cloning and immunological characterization of rabbit p53.

A:Reference number: JC6193; MUID:97208869
A:Accession: JC6193
A:Molecule type: mRNA
A:Residues: 1-391 <LEA>
A:Cross-references: EMBL:X90592; NID:91532043; PIDN:CAA62216.1; PID:e194962; PID:g153
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: tumor

Query Match 21.4%; Score 724.5; DB 2; Length 391;
Best Local Similarity 43.5%; Pred. No. 3.4e-43;
Matches 165; Conservative 54; Mismatches 103; Indels 57; Gaps 10;

QY 21 SLEP---DSTYFDLPQSSRGNEVGGTDSMDVFHLEGTTTSMVAFNLSSTMDQSS 77
DB 9 SLEP---DSTYFDLPQSSRGNEVGGTDSMDVFHLEGTTTSMVAFNLSSTMDQSS 77

QY 78 RAASAPYTPPEHAASVP-THSPYAPQSTFDTMSPAPV-----IPSNIDYPGPHFE 128
DB 49 -VANLNEDPEGLRVPAAPAPAPAPAPAPAPATSWPLSSSVPSQKTYHGNVGR 107

QY 129 VTFQSSSTAKSATWTYSPLKLYCQIAKTCPIQIKVSTPPPGTATIRAMPYKKAHV 188
DB 108 LGLFHSFGTAKSVTCTYSPCLNKLFCQIAKTCPIQLWSTPPPGTATIRAMPYKKAHV 167

QY 189 DYVKRCPNHELGRDFNEGQSPASHLRVSGNLSQYVDDPVTGRQSVVVPYEPVQVGT 248
DB 168 EVVRCPPHERCSD-SDG-LAPPOHLIRVSGNRAEYLDROTFRHSVVPYEPVQVGT 225

QY 249 FTIILYNFMCNCCVGGNRRPILITILEMRDQGVLRGRSTFGRKADHDHREOQ 308
DB 226 CTTIHYNFCNCCVGGNRRPILITILEMRDQGVLRGRSTFGRKADHDHREOQ 285

QY 309 YEQALNNESSAKNG-----AASKRAKQSPAPVAPALGAGVKKRRHDETYVLOVR 360
DB 286 FR-----KKEGCPPELPQSSSKRAL-----PTTTDSSPQTKKPLDGEYFLKIR 331

QY 361 GRENPELMLKESLELME 379
DB 332 GREPFEMFELNEALELKD 350

RESULT 9
DNH033
cellular tumor antigen p53 - human
N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation supp
C:Species: Homo sapiens (man)
C:Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
C:Accession: A25224; A43073; J0436; S40773; S42669; A22837; A5060; A25397; B25397;
4805; I58354; I78850; I52681; S60153
R:Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986
A:Title: Characterization of the human p53 gene.
A:Reference number: A25224; MUID:87064416
A:Accession: A25224
A:Molecule type: DNA
A:Residues: 1-393 <LAW>
A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1;
R:Chuman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
Gene 70, 245-252, 1988
A:Title: A variation in the structure of the protein-coding region of the human p53 g
A:Reference number: J0436; MUID:89108008
A:Accession: A43073
A:Molecule type: DNA
A:Residues: 1-393 <BUC1>
A:Cross-references: EMBL:M22898; NID:g189474
A:Note: This 72-Arg allele appears to be about 5 times more frequent than the 72-Pro
A:Accession: J0436
A:Molecule type: DNA
A:Residues: 1-71; 'P', 73-393 <BUC2>
A:Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476

A:Molecule type: mRNA
A:Residues: 1-393 <RIG>
A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho; F;176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;176,179,238,242/Binding site: zinc (Ser, His, Cys, Cys) #status predicted
F;392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.2%; Score 718.5; DB 1; Length 393;
Best Local Similarity 42.1%; Pred.No.9e-43;
Matches 160; Conservative 58; Mismatches 103; Indels 59; Gaps 11;

QY 14 TFEHLKSSLEPDSTYFDLPSSRGNNVVGTTSDSMDVFHLEGMTTSVMAQFNLLSSTD 73
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 18 TFSDLKLLENVNVLSPLSQA-----VDLM-----LSPDDLAAQW-LTEDPGP 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 QMSRAASASPTEHAASVPTHSPIVAQPSSTDTTWSAP-----VIPSENTDYPGPHHF 127
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 DEAPRMSEAAP----EMAPTFAAPTAA-----APAFSWPLSSVSPSKTYHGSGF 109
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 128 EVTFQQSSTAKSATWTYSPLLKLYCQIAKTCTCIQIKVSTPPPTTAIRAMPVYKKAEHV 187
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 110 RLGLFHSGTAKSVTCYISPOLNMFCQLAKTCPQVLWDSTPPGSEVRAMAIYKQSQHM 169
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 188 TDVVKCPNHRLGRDFNEGOSAPASHLRVEGNLSQYDDPVTGROSVVVPPEPOGT 247
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 170 TEVVRCPHERCSD-SDG-LAPPQHILIRVEGNLRVEYSDDRNTFRHSVVVPPEPVGS 227
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 248 EFTIILYNFNCNSCVGGMNRRLIIITILEMRDGOVLGRSFEGRTACPCGRDKADE 307
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 DCTTIHYNYCNWSCMGMMNRRLIITILEDSSGNLLGRNSEFVRVCACPGRRRTEE 287
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 308 HYREQALNESSAKNG-----AASKRAFKOSPAPPALGAGVKRRHRGDDETTYLQV 359
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 288 NFR-----KKGPCHELPGSTKRALPNNTSSPQ-----PKKKPLDGEYFTLQI 332
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 RGRNFELMKLESLEME 379
|||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 333 RGRERFEMFRELNEALEKD 352
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
DNMS53
cellular tumor antigen p53 - mouse
N/Alternate names: oncoprotein p53
C/Species: Mus musculus (house mouse)
C/Date: 28-Aug-1985 #sequence revision 04-Oct-1996 #text_change 22-Jun-1999
C/Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R/Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A/Reference number: A22739; MUID:85027173
A/Accession: A22739
A/Molecule type: DNA
A/Residues: 1-134,'V',136-390 <BIE>
A/Cross-references: GB:X00876; NID:g871420; PIDN:CAA35420.1; PID:g871421; GB:X01237;
R/Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
A/Rifle: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
A/Reference number: S06336; MUID:88221682
A/Accession: S06336
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-134,'V',136-390 <CHU>
R/Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.
Nature 306, 594-597, 1983
A/Rifle: A single gene and a pseudogene for the cellular tumour antigen p53.
A/Reference number: A02684; MUID:84068204
A/Accession: A02684
A/Molecule type: mRNA
A/Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 <ZAK>
A/Cross-references: GB:X01237; GB:X01700; NID:953575
R/Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640
A:Accession: S38822
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-390 <ARA1>
A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199
A:Accession: S38823
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167, 'G', '169-233', 'I', '235-390' <ARA2>
A:Cross-references: EMBL:M13873
R:Araki, N.; Nomura, K.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
submitted to the EMBL Data Library, July 1988
A:Reference number: S40014
A:Accession: S40014
A:Molecule type: mRNA
A:Residues: 1-167, 'G', '169-390' <ARA3>
A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201
R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the p53 protein.
A:Reference number: I48703; MUID:84272240
A:Accession: I48703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-47, 'R', '49-78', 'OW', '82-390' <RES>
A:Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA5323.1; PID:g53571
C:Comment: This DNA-binding protein plays an essential role in the regulation of cell division. The tetramer association region may exhibit a beta-turn, beta-sheet, beta-turn.
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:267-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.0%; Score 711.5; DB 1; Length 390;
Best Local Similarity 43.2%; Pred. No. 2.7e-42;
Matches 159; Conservative 64; Mismatches 104; Indels 41; Gaps 12;

QY 14 TFEHLNSSLPEPDSYFDLPQSSRGNNVGGTDSMDVPHLEGMTSVMAQFNLLSSTD 73
DB 21 TFGSLWKLPPE-----DILPSPHCMDLLLPQD--VEEF-FEGPSEAL----- 62

QY 74 QMSRRAASAPY--TPEHAASVPHSPYAPQSPSTFTDMSAPVIPNTDYPGPHHEVTF 131
DB 62 RVSGAPAAQDPVTETPGVPAPAPA-TPW--PLSSF-----VPSQKTYQNGYGFHLGF 110

QY 132 QQSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPYKKAHVTDV 191
DB 111 LQSGTAKSVNCTYSPPLNKLFCQIAKTCPIQIKVSTPPPPGTAIRAMPYKKAHVTDV 170

QY 192 KRCPNHELGRDNEGQAPASHLIRVEGNLSQYVDDPVTGQSVVVPYEPQVGEFTT 251
DB 171 RCPHERSCD-GDG-LAPQHLIRVEGNLYPEYLEDQCTFHSVVVVPYEPPEAGSYTT 228

QY 252 ILYNFCNCSVCGMNRRLPILITLEDMDGQVLGRSFEGRICACPGDRKADDEHYE 311
DB 1 ILYNFCNCSVCGMNRRLPILITLEDMDGQVLGRSFEGRICACPGDRKADDEHYE 311

DB 229 IHTYMCNCSMGMNRRPILITLEDSSGNLGRDSFEYRVVCACPGDRRTEENFRK 288
QY 312 QOALNESSAKNGAASRAKFPAPVAPALGAGVKRRKHGDEDTYVLOVGRNEFEILMKL 371
DB 289 KEVLCPELPGSA--KRALPTCTASAPP-----QKKKPLDGEYFTLKIRGRKREMFREL 341
QY 372 KESLELME 379
DB 342 NEALELKD 349

RESULT 12
S38824
Cellular tumor antigen p53, minor splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38824; S35478
R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640
A:Accession: S38824
A:Molecule type: mRNA
A:Residues: 1-381 <ARA>
A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
R:Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A:Title: Alternatively spliced p53 RNA in transformed and normal cells of diffuse large B-cell lymphoma.
A:Reference number: S35478; MUID:92253421
A:Accession: S35478
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-381 <HANA>
A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1992.
C:Comment: This sequence, produced by alternative splicing of the tenth intron, is not known.
C:Superfamily: cellular tumor antigen p53
C:Keywords: alternative splicing; phosphoprotein; zinc
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:267-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match 20.7%; Score 702; DB 2; Length 381;
Best Local Similarity 41.3%; Pred. No. 1.2e-41;
Matches 164; Conservative 69; Mismatches 114; Indels 50; Gaps 14;

QY 14 TFEHLNSSLPEPDSYFDLPQSSRGNNVGGTDSMDVPHLEGMTSVMAQFNLLSSTD 73
DB 21 TFGSLWKLPPE-----DILPSPHCMDLLLPQD--VEEF-FEGPSEAL----- 62

QY 74 QMSRRAASAPY--TPEHAASVPHSPYAPQSPSTFTDMSAPVIPNTDYPGPHHEVTF 131
DB 62 RVSGAPAAQDPVTETPGVPAPAPA-TPW--PLSSF-----VPSQKTYQNGYGFHLGF 110

QY 132 QQSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPYKKAHVTDV 191
DB 111 LQSGTAKSVNCTYSPPLNKLFCQIAKTCPIQIKVSTPPPPGTAIRAMPYKKAHVTDV 170

QY 192 KRCPNHELGRDNEGQAPASHLIRVEGNLSQYVDDPVTGQSVVVPYEPQVGEFTT 251


```
Db 171 RRCPHHRCSD-GDG-LAPQHLIRVEGNYLEYLEDQTFHSHVYVYEPPEAGSEYTT 228
QY 252 ILYNFMNCSSCVGMNRRPILITILEMRDGOVLGRSPEGRICACPGDRKADREHYRE 311
Db 229 IHXYMNCSSCMGMNRRPILITILEDSGNLLGRDSFEVACACPGDRRTTEENFRK 288
QY 312 QOALNESSANGAASKRAFQKSPAPVAGAGVKKRRHGDDETYLYQVGRNFEILMKL 371
Db 289 KEVLCPELPFGSA--KRALPTCTASPP-----QKKPLDGEYFTLKIRGRKREMFREL 341
QY 372 KESELMELVPLQVDSYRQOQLQRP-SHLQPPSY 407
Db 342 NEALELK-----DAHATESGDSRAHSSLOPRAF 370

RESULT 13
I46226
p53 - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46226
R:Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.
Anticancer Res. 14, 2039-2046, 1994
A:Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.
A:Reference number: I46226; MUID:95150524
A:Accession: I46226
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-77 <DEV>
A:Cross-references: GB:L27630; NID:g508454; PIDN:AAC37327.1; PID:g508455
C:Genetics:
A:Gene: p53
A:Introns: 24/1: 61/3
C:Superfamily: cellular tumor antigen p53

Query Match 7.3%; Score 248.5; DB 2; Length 77;
Best Local Similarity 61.5%; Pred. No. 5e-11;
Matches 48; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

QY 183 KAEHYDVYKRCNHELGRDFNEGOSAPASHLIRVEGNLSQYVDDPVTGQSVVYVPEP 242
Db 1 KSEFVTEVYVRCPPHRCSDSDG-LAPPOHLIRVEGNLRAKYLDRTYFRHSVYVPEP 59
QY 243 POGTEFTILYNFMNCS 260
Db 60 PEVGFDTYTHNYMCS 77

RESULT 14
T00074
hypothetical protein KIAA0460 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 07-May-1999
C:Accession: T00074
R:Seiki, N.; Ohira, M.; Negase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A:Reference number: Z14085; MUID:98116662
A:Accession: T00074
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-903 <SEK>
A:Cross-references: EMBL:AB007929; NID:d1225338; PID:d1033267
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0460

Query Match 4.5%; Score 151.5; DB 2; Length 903;
Best Local Similarity 21.1%; Pred. No. 0.0086;
Matches 175; Conservative 75; Mismatches 253; Indels 327; Gaps 45;
```

```
QY 3 QSTATSPD-----GGTTFEHL-----WSSLEPDSYFDLPQSSRGNNNEVVGTD 46
Db 102 ESESTSPLEMKIHNFLKGNPGSGLNLPILSSLGSA-----PSESHPSDFORGPTS 156
QY 47 SMDVFLHEGM-----TTSVMAQFNLLSSTMDQMSRAASA-SP-- 85
Db 157 TSID--NIDGTPVDRSGTPTODMMDKPTSSVDTMSLLKIIISPGSSTPSSTRSPPP 214
QY 85 -----YYPEHAASVPTH-----SPYAOPTSTFTDMSAPVIPSNT----- 120
Db 215 GRDESYPRELSNSVYRPFGLSGSESYKQPSDGM-----RPSSLMDSQKFPDTSFQD 272
QY 120 -----DYPGPHFEVTFQOSSTAKSA-----TWYSPLKLYCQIAKTCPIQIKV 165
Db 273 EDYRDFEYSGPPPSAMNLEKPAKSLKSLSDTEYQPIILSS-YSHRAQ--EFGVKS 329
QY 166 STPPPGTAIRAMPVYKKAHVTDVVKRCP-----NHELGRD-----FN 204
Db 330 AFPP-----SVRAL-----LDSENCDRLSSPGLFGAFSVRGNFSGDRSPSPSKN 376
QY 205 EGOSAPASHLIRVEGNLS-----QYVDDP-----VTGROSVVVPY-EPP 243
Db 377 DSFTTPDSN-----HNSLSOSTTGHLSLPQKQYDPSHPVPHRSLSFPQNTLAAPTGHPP 431
QY 244 QVGTFTTILYNFMNCSVCYGMN-----RRPILIIILEMRDGOVLGRSFEGRIC-- 296
Db 432 TSGVE--KVLASTISTTSTIEFKNMLKNASRKP-----SDDKHFGQAPSKGTPSDG 480
QY 296 -----ACPGDRKRADEHYREQA-----LNSSAKNGA-----ASKRAF 330
Db 481 VLSNLNQPISLATDQOQEEHYRIETRVSSCLDLPDSTEKGAPIETLGYHSASNRN 540
QY 331 KQSP-----PAVPALGAGVKRRHGDDEDT-----YYQVGRNFEILMKLESLEL----- 378
Db 541 SGEPIOTVESIRVPGKG--NRGHGREASRVGWFDLSTSGSFDNGPSSASELASLGGGGS 598
QY 378 -----MELVP--QPLVDSYRQOQLQRP-SHLQ-----PSYGP 409
Db 599 GGLTGFTATYKERAQFQBSVGSFRNSFNSTFEHLLPSPLEHGTFFQREPVPGPSAP 658
QY 410 VLSPMNVHGM-----NKLPSVN-----QLVGQPPPHSSAATNLGVPVGP 451
Db 659 PVPP--KDHGGIFSDAPTHLPVSLNSFTKEAALAHAAAPPPPGHSGIPIPTPPP- 716
QY 452 MLNNHGHAVPANGEMSSSHSAQSMVSGSHCTPPPHADPSLVSP-----LTGLGCPNCIE 507
Db 716 -----PPPGHSS--SGSGGVFPSTPPPPPPVDSHGVVFPAPPPLAEHGVAGAVA 764
QY 508 YFTSQGLQSIYH---LQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHDIYSTAQQLRSS 564
Db 765 VFPKD-----HSSLQGLTAEHFGVLP-----RDHGGPTQ--RDL 799
QY 565 NAATISGGSELQORVMEVHFVRVHITIPN-----RGPGGG 605
Db 800 NGPGLS-----RVRESLTLPSSHLEHLGPPHGGGGG 831

RESULT 15
T04518
hypothetical protein F16A16.80 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04518
R:Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheisel, J.; M
submitted to the Protein Sequence database, February 1999
A:Reference number: Z15376
A:Accession: T04518
A:Molecule type: DNA
A:Residues: 1-864 <BEV>
A:Cross-references: EMBL:AL035353
A:Experimental source: cultivar Columbia; BAC clone F16A16
C:Genetics:
```


A:Map position: 4
A:Note: Intron positions not resolved
A:Note: F16A16.80

```

Query Match      4.3%; Score 145; DB 2; Length 864;
Best Local Similarity 17.7%; Pred. No. 0.023;
Matches 100; Conservative 83; Mismatches 207; Indels 174; Gaps 22;

QY 95 THSPYAPQPSSTFTMSAPVIP--SNTDY-----PQP 124
Db 91 TSTPATHQSSVSLPPPIIAPYISGLDFGLGVKMMWNSYGAASKFASRHRDPFL 150
QY 125 HFEVTFQSSSTAKSATWYSPLKLYCO-IAKTCPIQKVS-----TPPPPGTAIRAM 178
Db 151 LPSAAAEVGEDEMASWLYHPLRQDYFSSGVASTSATPQSSASLAPTPPPSPVYGOI 210
QY 179 PVYKAEHVTDVVKRCFNHELGRDFNEG--QSAPASHLIRVEGNLSQYVDDPVTGROSV 236
Db 211 PVERRTENFNNFLRL-----RGNIFSGRVEAGP---VVIETQIGSSATPSSAAESC 261
QY 237 VVYEPQVGTETTYLYNPMCNSSCVGGMNRPILIIITLEMRDGOVLGRR-----SFEQ 292
Db 262 VI---PATHTESRAAATGVSTFAVPGLGRR-----GKEYATETAGTSYSG 306
QY 293 -----RICACPRDRKKADEHYREQ--QALNESSAKNGAASKRAFKQSPPAVPALGAG 343
Db 307 VNKAETERVQIQPERTKITEDKKRETTAEIQGTAEAGSTSR----- 351
QY 344 VKRRRGDEDT-----YLVQVRGKRE-----NFEILMKLAKES 374
Db 351 -KRSRAADMHNLSEVLIIFYLETEGKQDREDENSARTPSSIQKDSNKGFKVSWKINAN 409
QY 375 L--ELMELVPOPLVDSYRQQQLQRPShLOPP-----SYGPVLSPMKNVHGGNKL 424
Db 410 LISHVLELITEILVIESMLLCQMSMGHGMPPMHGEGNTQQFNPMHMGWK---GMNRP 466
QY 425 PSYNQLVGOPPPHSSAATNLGPGVGMNLNNHGHAVPA-----NGEMSSSHSAQSNVSGSH 480
Db 467 PPEVPPFGKTFPR-----PGHMAGVGPSPYALRYFPDPDTQASDLRSRVHPSLH 514
QY 481 CTPPPYHADPSLVSELTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYMT 540
Db 515 SNVPNQPRFPAYIN-----PYSQFVGLHMQ-----QPPLPLQVI 550
QY 541 INRGLODLKQGHDIYTAQQLRSS 564
Db 551 LSOYLLPVNQHHSLVSATQVLASN 574

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Job time: 4490 sec